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Db 3335 CCCTGCCAGAAGGTATTTGTGGTGCAGCAGATTCCCAACAGTAACCTCCTTCCTCCTGGTG 3394

Qy 991 ThrAspProThrCysAspCysSerIlePhePheProProValLeuGlnValAlaThrGluVal 1010
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Qy 1011 LysTyrAsnAlaSerValLysCysAspArgMetArgSerGlnLysLeuArgArgPro 1030
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Qy 1031 AspSerCysHisAlaPheHisProGluValArgValAlaValAlaAspArgGlyTrpAlaGly 1050
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Db 3575 ACCTCAGCCTCGCCGCCGCCCTACTCCTGCT-GCCTGTGTGTCCTGGGGGCTACTGCCCCA 3633

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Qy 1071 MetProMetAsnThrPro 1076
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RESULT 4
AX098927
LOCUS   AX098927   3339 bp   DNA   linear   PAT 02-APR-2001
DEFINITION   Sequence 52 from Patent WO0119870.
ACCESSION   AX098927
VERSION   AX098927.1   GI:13538144
KEYWORDS   .
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS   Brown,J.P. and Bertelli,F.
TITLE   Secreted soluble _g(a)2_g(d)-2, _g(a)2_g(d)-3 or _g(a)2_g(d)-4
             calcium channel subunit polypeptides and screening assays using
             same
JOURNAL   Patent: WO 0119870-A 52 22-MAR-2001;
             WARNER-LAMBERT COMPANY (US)
FEATURES   Location/Qualifiers
source   1..3339
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
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ORIGIN

Alignment Scores:
Pred. No.:   0
Score: 5342.50   Length: 3339
Percent Similarity: 97.54%   Matches: 1028
Best Local Similarity: 97.35%   Conservative: 2
Query Match: 93.30%   Mismatches: 8
DB: 6   Indels: 18
                                                   Gaps: 2

US-09-833-222A-10 (1-1090) x AX098927 (1-3339)

Qy 11 AspArgValLysLeuTrpLeuAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
        ::: ||||
Db 174 GAAACAGTGAAGCTATGGCTGGCAGACCTTCGGCGGGACCTGTATAACACTGTGACCAAA 233

Qy 31 TyrSerGlySerLeuLeuLeuGlnLysGlyLysLysTyrLysAspValGluSerLeuLysIle 50
        ||||||||||||||||||||||||||||||||||||||||||||||
Db 234 TACTCAGGCTCTCTCTTGCTCCAGAAAGGTACAAGGATGTGGAGTCTCTGAAGATC 293

Qy 51 GluGluValAspGlyLysLeuGluLeuValArgLysPheSerGluAsnMetLeu 70
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 294 GAGGAGGTGGATGGCTTGGAGCTGGTGAGAAAGTTCTCAGAGAACATGCTG 353

Qy 71 ArgArgLysValGluValGlnAlaArgGluAlaLysLeuAsn 90
        ||||||
Db 294 GAGGAGGTGGATGGCTTGGAGCTGGTGAGAAAGTTCTCAGAGAACATGCTG 353

Qy 611 LeuHisProAspLeuAlaLeuAlaGlyAspTrpIleTyrCysIleThrAspIleAspPro 630
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Db 2255 CTTCACCCAGACCTGGCCCTGGCCGGTGACTGGATCTACTGCATCACAGATATTGACCCA 2314

Qy 631 AspHisArgLysLeuSerGlnLeuGluLeuAlaMetIleLeuArgPheLeuThrArgLysAspPro 650
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Db 2315 GACCACCGGAAGCTCAGCCAGCTAGAGCTGGCCATGATCCGCTTCCTGCCCAGGAAGGACCCCA 2374

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Qy 751 PheAsnLeuArgTrpAlaGlyGluGlyTyrProGluSerAlaGlyLyeProMetValValThrGlyArgAla 770
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Db 2675 TTCAACCTCCGCTGGGCAGGAGAAGGACCCAGAAGTGCCGGGTGAACCCATGGTGTGACCGGCA 2734

Qy 771 SerThrAlaValAlaValThrArgValAlaAspLysArgThrAlaIleAlaAlaAlaAlaAlaGlyValVal 790
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Db 2855 GTGGATGGGCCGTGCACACAGACTGCCGGGACAGTGATCTGCGAGTCTGGCTTCGTCATCGAC 2914

Qy 831 AsnAsnGlyPheIleLeuLeuSerLysArgSerArgGluThrGlyGlyGlyGluAlaGlyAsn 850
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Db 2915 AACAACGGGTTCATTCTGAATCTCTGAAGAGTCCCAGAGACGGGAAGATTTCTGGGGGAG 2974

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Db 2975 GTCAGCGCCAATTTCTGCCTTCTTGACCGTGCTGACCAGTGCGTTCAGCCAAGTGACTATG 3034

Qy 871 TyrAspTyrGlnIleAlaMetCysGlyLysProSerSerHisHisHisSerAlaAlaGlnProLeu 890
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Db 3275 TACCCCGTGTTCGTGTACCAGCCAGCGATCCGGGAGGCCCTAAATGGGATCATCGTGGAGGTGGAG 3334

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451 PheSerLysAsnGluThrArgSerHisGlyIleLeuLeuGlyValValGlySerAsp 470
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1494 TTCAGCAAGAAGAACGAAACGGATCCCCATGGCATTCTCTGGGTGTGTGGGTCTCAGAT 1553
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471 ValAlaLeuArgGluLeuMetLysGluAlaProArgTyrLysLeuGlyValHisGlyTyr 490
Qy
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Qy
1794 CTCTCGATGGATGTGAAGGTTCCGATGGATAAAGGGAAGGGAGTTCTTTTCCTGACCAAT 1853
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571 AspTyrPhePheThrAspIleSerAspThrProPheSerLeuGlyAlaValLeuSerArg 590
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591 GlyHisGlyLeuTyrIleLeuLeuGlyAsnThrSerValGluGlyLeuHisAspLeu 610
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1914 GGCCACGGACGATACATCCTTCTCGGGAACACGTCTGTGGAAGAGGCCTGCATGACTTG 1973

611 LeuHisProAspLeuAlaLeuLeuAlaGlyAspTrpIleCysTyrCysIleAspAspPro 630
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171 ValGluAsnPheGlyAsnArgGlnArgAspProThrLeuThrTrpThrTrpGlnThrTyrPheGlySerAlaThrGly 190
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654 GTGGAGAACTTCGGAGAGAGACCCACGTTGACCTGGACTTGGCAGACTTATTTTGGCAGTGCAACTGGA 713

191 PhePheArgIleTyrProGlyIleLeuLysTrpThrProAspGluAsnGlnAsnGlyValIleLeuThrPhe 210
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211 AspCysArgAsnArgGlyThrGlyTrpTyrTyrIleGlnIleAlaAlaThrSerProLysAspIleValIle 230
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Alignment Scores:
Pred. No.:   0   Length: 3339
Score: 5342.50   Matches: 1028
Percent Similarity: 97.54%   Conservative: 2
Best Local Similarity: 97.35%   Mismatches: 8
Query Match: 93.30%   Indels: 18
DB: Gaps: 2

US-09-833-222A-10 (1-1090) x AX099347 (1-3339)

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Qy      11 AspArgValLysLeuTrpAlaAspThrPheGlyGlyAspLeuTyrAsnThrValThrLys 30
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Db     174 GAAACAGTGAAGCTATGGGCTGACACCTTCGGCGGGGACCTGTATAACACTGTGACCAAA 233

Qy      31 TyrSerGlySerLeuLeuLeuGlnLysLysTyrLysAspValGluSerLeuLysIle 50
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      91 HisGluAsnGluSerLeuValPheAspTyrTyrAsnSerValLeuIleLeuAsnGluArg 110
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Qy     131 PheSerAsnLeuProValAsnThrSerIleSerSerValGlnLeuProThrAsnValTyr 150
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Qy     151 AsnLysAspProAspIleLeuAsnGlyValTyrMetSerGluAlaLeuAsnAlaAlaPhe 170
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Qy     231 LeuValAspValSerMetLysGlySerMetThrIleAlaLysHisThrIle 250
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Qy     834 eIleLeuIleSerLysArgArgGluThrGlyThrArgPheLeuGlyLeuGluValAspGlyAl 854
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Qy     994 rCysAspCysSerIlePheProProValLeuGlnValAlaThrGluValLysTyrAsnAl 1014
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Qy    1014 aSerValLysCysAspAspArgMetArgSerGlnLysLeuLeuArgArgArgAspSerCysHi 1034
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RESULT 5
LOCUS   AX099347   3339 bp   DNA   linear   PAT 02-APR-2001
DEFINITION Sequence 52 from Patent WO0120336.
ACCESSION   AX099347
VERSION   AX099347.1 GI:13538490
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bertelli,F., Brown,J.P., Dissanayake,V., Suman-Chauhan,N. and
            Gee,N.S.
  TITLE   Screening for alpha2delta-1 subunit binding ligands
  JOURNAL   Patent: WO 0120336-A 52.22-MAR-2001;
            WARNER-LAMBERT COMPANY (US)
FEATURES   Location/Qualifiers
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                     /mol_type="unassigned DNA"